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===============================================================
Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Wed Oct 10 10:48:32 EDT 2007
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Reviewer Comments:
<110> APPLICANT: Brockhaus, et al.
<120> TITLE OF INVENTION: Human TNF Receptor
<130> FILE REFERENCE: 01017/40451C
<140> CURRENT APPLICATION NUMBER: US/08/444,790A
<141> CURRENT FILING DATE:  1995-05-19
<150> PRIOR APPLICATION NUMBER: CH 3319/89
<151> PRIOR FILING DATE: 1989-09-12

The above is a sample of global errors:  please do not include the
alphabetical headings next to the numeric identifiers:  just use the
numeric identifiers and their responses (e.g., <110> Brockhaus, et al.).
 Also, please remove the "A" at the end of the <140> response (should
just be US/08/444,790).
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Validated By CRFValidator v 1.0.3

Application No: 08444790   Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-20 18:09:44.546
Finished: 2007-09-20 18:09:45.706
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 160 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 26
Actual SeqID Count: 26

Error code   Error Description

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              Input Set:


             Output Set:



               Started:   2007-09-20 18:09:44.546
              Finished:   2007-09-20 18:09:45.706
               Elapsed:   0 hr(s) 0 min(s) 1 sec(s) 160 ms
       Total Warnings:    22
         Total Errors:    0
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   Actual SeqID Count:    26
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Error code   Error Description

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<211> LENGTH: 2111

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

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<211> LENGTH: 455
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
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        Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
                    20                  25                  30
        His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
                35                  40                  45
        Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
            50                  55                  60
        Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
        65                  70                  75                  80
        Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
                        85                  90                  95
        Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
                    100                 105                 110
        Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
                    115                 120                 125
        Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
            130                 135                 140
        Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
        145                 150                 155                 160
        Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                        165                 170                 175
        Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
                    180                 185                 190
        Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
                    195                 200                 205
        Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
            210                 215                 220
        Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
        225                 230                 235                 240
        Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
                        245                 250                 255
        Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
                    260                 265                 270
        Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
                    275                 280                 285
        Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
            290                 295                 300
        Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
        305                 310                 315                 320
        Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
                    325                 330                 335
        Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
                    340                 345                 350
        Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
                    355                 360                 365
        Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
            370                 375                 380
        Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
```

```
            385                     390                     395                     400
        Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
                         405                     410                     415
        Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
                     420                     425                     430
        Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
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        Pro Ala Pro Ser Leu Leu Arg
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```

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<211> LENGTH: 2339
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 3
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    actcgggaac agaaccgcat ctgcacctgc aggcccggct ggtactgcgc gctgagcaag     180
    caggaggggt gccggctgtg cgcgccgctg ccgaagtgcc gcccgggctt cggcgtggcc     240
    agaccaggaa ctgaaacatc agacgtggtg tgcaagccct gtgccccggg gacgttctcc     300
    aacacgactt catccacgga tatttgcagg ccccaccaga tctgtaacgt ggtggccatc     360
    cctgggaatg caagcaggga tgcagtctgc acgtccacgt cccccacccg gagtatggcc     420
    ccaggggcag tacacttacc ccagccagtg tccacacgat cccaacacac gcagccaagt     480
    ccagaaccca gcactgctcc aagcacctcc ttcctgctcc caatgggccc cagcccccca     540
    gctgaaggga gcactggcga cttcgctctt ccagttggac tgattgtggg tgtgacagcc     600
    ttgggtctac taataatagg agtggtgaac tgtgtcatca tgacccaggt gaaaaagaag     660
    cccttgtgcc tgcagagaga agccaaggtg cctcacttgc ctgccgataa ggcccggggt     720
    acacagggcc ccgagcagca gcacctgctg atcacagcgc cgagctccag cagcagctcc     780
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    tcttcccctg gtggccatgg gacccaggtc aatgtcacct gcatcgtgaa cgtctgtagc     960
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    tctgcccagc tctggcttcc agaaaacccc agcatccttt tctgcagagg ggctttctgg    1620
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    tcacgcctat gatcccagca ctttgggagg ctgaggcggg tggatcacct gaggttagga    1860
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    gccgggcgtg gtggcgggca cctatagtcc cagctactca gaagcctgag ctgggaaat     1980
    cgtttgaacc cgggaagcgg aggttgcagg gagccgagat cacgccactg cactccagcc    2040
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    catattcagt gctgtggcct gggcaagata acgcacttct aactagaaat ctgccaattt    2220
    tttaaaaaag taagtaccac tcaggccaac aagccaacga caaagccaaa ctctgccagc    2280
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<211> LENGTH: 392
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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 4

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            20                  25                  30
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
        35                  40                  45
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
    50                  55                  60
Arg Leu Cys Ala Pro Leu Pro Lys Cys Arg Pro Gly Phe Gly Val Ala
65                  70                  75                  80
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
                85                  90                  95
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
            100                 105                 110
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
            115                 120                 125
Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
    130                 135                 140
His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Ser
145                 150                 155                 160
Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
                165                 170                 175
Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val
            180                 185                 190
Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val
            195                 200                 205
Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu
    210                 215                 220
Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly
225                 230                 235                 240
Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser
                245                 250                 255
Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala
            260                 265                 270
Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala
            275                 280                 285
Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Ala Asp Ser Ser Pro Gly
    290                 295                 300
Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser
305                 310                 315                 320
Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
            325                 330                 335
Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val
            340                 345                 350
Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
            355                 360                 365
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Pro Asp Ala Gly Met Lys Pro Ser
385                 390
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<210> SEQ ID NO 5
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<212> TYPE: PRT

<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (25)..(25)
<223> OTHER INFORMATION: Xaa = any or unknown amino acid
<400> SEQUENCE: 5
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      Gln Gly Lys Tyr Ile His Pro Glu Xaa Asn Ser Ile
                      20   25

<210> SEQ ID NO 6
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic peptide
<400> SEQUENCE: 6
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<210> SEQ ID NO 7
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<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic peptide
<400> SEQUENCE: 7
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      1   5   10   15
      Pro Leu

<210> SEQ ID NO 8
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic peptide
<400> SEQUENCE: 8
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<210> SEQ ID NO 9
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic peptide
<400> SEQUENCE: 9
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      1   5   10   15

<210> SEQ ID NO 10
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<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (8)..(8)

<223> OTHER INFORMATION: Xaa = any or unknown amino acid

<400> SEQUENCE: 10

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1               5                   10                  15
Thr Cys
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<210> SEQ ID NO 11

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (2)..(2)

<223> OTHER INFORMATION: Xaa = any or unknown amino acid

<400> SEQUENCE: 11

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<210> SEQ ID NO 12

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 12

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<210> SEQ ID NO 13

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 13

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<210> SEQ ID NO 14

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (9)..(10)

<223> OTHER INFORMATION: Xaa = any or unknown amino acid

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (13)..(13)

<223> OTHER INFORMATION: Xaa = any or unknown amino acid

<400> SEQUENCE: 14

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```

<210> SEQ ID NO 15

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 15

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<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic primer

<400> SEQUENCE: 16

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<210> SEQ ID NO 17

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic primer

<400> SEQUENCE: 17

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